

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/576,051A  
Source: IFWP  
Date Processed by STIC: 1/19/07

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 01/19/2007

PATENT APPLICATION: US/10/576,051A

TIME: 09:59:56

Input Set : A:\PN-4-33424A-USN-Sequence-Listing-ST25-Final-Version.txt

Output Set: N:\CRF4\01192007\J576051A.raw

3 <110> APPLICANT: Novartis AG et al.  
 5 <120> TITLE OF INVENTION: GENES INVOLVED IN NEURODEGENERATIVE DISORDERS  
 7 <130> FILE REFERENCE: PN/4-33424A/USN  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/576,051A  
 C--> 10 <141> CURRENT FILING DATE: 2006-04-18  
 12 <150> PRIOR APPLICATION NUMBER: US60/513241  
 13 <151> PRIOR FILING DATE: 2003-10-22  
 15 <160> NUMBER OF SEQ ID NOS: 40  
 17 <170> SOFTWARE: PatentIn version 3.2  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 2781  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: misc\_feature  
 26 <222> LOCATION: (546)..(546)  
 27 <223> OTHER INFORMATION: n is a, c, g, or t  
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 34 cgccctttgtc ttcccgcctc ccccttcctt tttcaaaagc caagaggtaa ttatttggtc 180  
 36 tttgtgcaag gcaaacctct ccagatgcca cttccaaata taggctctca ttaacaccag 240  
 38 aggctggcct ggtgtggtgc agggcgggccc ttccttctcc tggcggacac tgtgtccccg 300  
 40 cgcgctggcg ctgcaccaca tctggaagcc aggcgggcag ggcagagacc ccggctcctg 360  
 42 cgcccctcct agtcccaga gagcgtggat cgcgggcggg gctcaccgag cgaggttacc 420  
 44 tctcttgaaa atacttaaac actttttttc ctctccactg aaatctcaaa aaacagccca 480  
 46 ttttgaacca gaataattta gtctgacaac agattcttcc tctgttcaca gctgtcccag 540  
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 50 aaaaaaaaaa cctcccagcc aaaacgggct cagttcgtaa aggagccggg tgacttcaga 660  
 52 ggcgccggcc cgctccgtctg ccgcacctga gcacggcccc tgcccagacc tggcccggcg 720  
 54 cgatgctgta gggaccgccc tgctcctccc ccggaccggt atccgcgccc ggcgcccggc 780  
 56 agaccgctg gcaagatgcc gcgctccttc ctggtcaaga agcatttcaa cgctccaaa 840  
 58 aagccaaact acagcgaact ggacacacat acagtgatta tttcccgcga tctctatgag 900  
 60 agttactcca tgctgtcat accacaacca gagatcctca gctcaggagc atacagcccc 960  
 62 atcactgtgt ggactaccgc tgctccattc cagccccagc tacccaatgg cctctctcct 1020  
 64 ctttccggat actcctcatc tttggggcga gtgagtcccc ctctccatc tgacacctcc 1080  
 66 tccaaggacc acagtggctc agaaagcccc attagtgatg aagaggaaag actacagtcc 1140  
 68 aagctttcag acccccattg cattgaagct gaaaagtctc agtgcaattt atgcaataag 1200  
 70 acctattcaa ctttttctgg gctggccaaa cataagcagc tgactgcga tgcccagtct 1260  
 72 agaaaatctt tcagctgtaa atactgtgac aaggaatatg tgagcctggg cgccctgaag 1320  
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 78 cctcactgca acagagcatt tgcagacagg tcaaatctga gggctcatct gcagacccat 1500

(Pg. 6)

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82 ctgcacaaac atgaggaatc tggctgctgt gtagcacact gagtgacgca atcaatgttt 1620
84 actcgaacag aatgcatttc ttcactccga agccaaatga caaataaagt ccaaaggcat 1680
86 tttctcctgt gctgaccaac caaataatat gtatagacac acacacatat gcacacacac 1740
88 acacacacac ccacagagag agagctgcaa gagcatggaa ttcattgtgt taaagataat 1800
90 cctttccatg tgaagtttaa aattactata tatttgctga tggctagatt gagagaataa 1860
92 aagacagtaa cctttctctt caaagataaa atgaaaagca cattgcatct tttcttccta 1920
94 aaaaaatgca aagatttaca ttgctgccaa atcatttcaa ctgaaaagaa cagtattgct 1980
96 ttgtaataga gtctgtaata ggatttccca taggaagaga tctgccagac gcgaactcag 2040
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102 aaaaaaataa caagaacaaa acacaggaga atgtattaaa agtatttttg ttttgttttg 2220
104 tttttgccaa ttaacagtat gtgccttggg ggaggaggga aagattagct ttgaacattc 2280
106 ctggcgcatg ctccattgtc ttactatttt aaaacatttt aataattttt gaaaattaat 2340
108 taaagatggg aataagtgca aaagaggatt cttacaaatt cattaatgta cttaaactat 2400
110 ttcaaagtca taccacaaat gcaataatac aatacccctt ccaagtgcct ttttaaattg 2460
112 tatagttgat gagtcaatgt aaatttgtgt ttatttttat atgattgaat gagttctgta 2520
114 tgaaactgag atgttgtcta tagctatgtc tataaacaac ctgaagactt gtgaaatcaa 2580
116 tgtttctttt ttaaaaaaca attttcaagt tttttttaca ataaacagtt ttgatttaaa 2640
118 atctcgtttg tatactattt tcagagactt tacttgcttc atgattagta ccaaaccact 2700
120 gtacaaagaa ttgtttgtta acaagaaaaa aatgaataat gcttattatg catctgaagt 2760
122 gttattttat gtgtagatt a 2781
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 268
127 <212> TYPE: PRT
128 <213> ORGANISM: Homo sapiens
130 <400> SEQUENCE: 2
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136 Pro Asn Tyr Ser Glu Leu Asp Thr His Thr Val Ile Ile Ser Pro Tyr
137 20 25 30
140 Leu Tyr Glu Ser Tyr Ser Met Pro Val Ile Pro Gln Pro Glu Ile Leu
141 35 40 45
144 Ser Ser Gly Ala Tyr Ser Pro Ile Thr Val Trp Thr Thr Ala Ala Pro
145 50 55 60
148 Phe His Ala Gln Leu Pro Asn Gly Leu Ser Pro Leu Ser Gly Tyr Ser
149 65 70 75 80
152 Ser Ser Leu Gly Arg Val Ser Pro Pro Pro Pro Ser Asp Thr Ser Ser
153 85 90 95
156 Lys Asp His Ser Gly Ser Glu Ser Pro Ile Ser Asp Glu Glu Glu Arg
157 100 105 110
160 Leu Gln Ser Lys Leu Ser Asp Pro His Ala Ile Glu Ala Glu Lys Phe
161 115 120 125
164 Gln Cys Asn Leu Cys Asn Lys Thr Tyr Ser Thr Phe Ser Gly Leu Ala
165 130 135 140
168 Lys His Lys Gln Leu His Cys Asp Ala Gln Ser Arg Lys Ser Phe Ser
169 145 150 155 160
172 Cys Lys Tyr Cys Asp Lys Glu Tyr Val Ser Leu Gly Ala Leu Lys Met
173 165 170 175

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176 His Ile Arg Thr His Thr Leu Pro Cys Val Cys Lys Ile Cys Gly Lys
177                               180                     185             190
180 Ala Phe Ser Arg Pro Trp Leu Leu Gln Gly His Ile Arg Thr His Thr
181                               195                     200             205
184 Gly Glu Lys Pro Phe Ser Cys Pro His Cys Asn Arg Ala Phe Ala Asp
185                               210                     215             220
188 Arg Ser Asn Leu Arg Ala His Leu Gln Thr His Ser Asp Val Lys Lys
189 225                               230                     235             240
192 Tyr Gln Cys Lys Asn Cys Ser Lys Thr Phe Ser Arg Met Ser Leu Leu
193                               245                     250             255
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200 &lt;210&gt; SEQ ID NO: 3

201 &lt;211&gt; LENGTH: 4325

202 &lt;212&gt; TYPE: DNA

203 &lt;213&gt; ORGANISM: Homo sapiens

205 &lt;400&gt; SEQUENCE: 3

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208 taatctcccc cttggtgcag ctgcttttga agtgagtttc ctgccagag ccccggtg      120
210 acacgcagcg gctcgcatcg cagagcgcag cgccggcgcg gggccgcgag aacgcagcgc      180
212 aggggagcag cccgaggcgg acaccgcgag ccgccggca ctccgcagt ccagccggct      240
214 cctctagccc ggccacggct ccgctgcggg ccaccagga ttactcgcgt ctggctccag      300
216 gcgccgagaa ggcgcgctgg gcgcccgtgg ccgccgcgcc agctcctcct cctcccgctg      360
218 ctctgtctcc cggggcgagc gcgcagcccc gagcccgccc cgcgcctccc ggagccctcc      420
220 ccccgctgc tcccatgcgc gcgggtgggt catgagcaca gcgccctcgc tttctgccct      480
222 aagaagcagt aagcacagcg gcggcgggcg cggcggaggc ggaggcggcg gtgcagaccc      540
224 tgcctggacc agcgcgctct ctggaaatag ctccggcccc ggcccaggct cgtccccggc      600
226 cggcagcacc aagccttttg tgcacgccgt gccccctct gacccctgc gccaggccaa      660
228 ccgcctgcc aatcaaggtgc tgaagatgct gacggcacga actggccaca ttttgcaccc      720
230 cgagtacctg cagccctgc cttccacgcc ggtcagcccc atcgaggtaa ggaccctctc      780
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236 cttccgtacc tcaaaactag ggcggaaaag ggggaggaag tggaatgggg cgtgcatgct      960
238 agggagcaag gctgccaaata cttgtttctc ctttcgatat gaaagccctt accccgacct      1020
240 aggcccttc actcggcacc gaaggcaggc ggaggctctga aatacggttc caaagtcgcc      1080
242 gtccttcgta tccgcagaag ccagtgtgtg cacacagcct ctgaggcgcc agccgcccga      1140
244 gcccttactc tgaagaatta aggagtgttt gtggggaggg ggtacagttc tgggtctagg      1200
246 aaccgaaaac caaaacattt tgctctttaa aaatctagtt agcgctcaga gagggcagga      1260
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250 gagaatgttt gtgagtgggt gttgaagagg ggggtgccgc tagaattgcg ccttgggggt      1380
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260 ccggcggcgg tgctgcgggc gacaaggaca ccaaatcggg cccctgaag ctgagcgaca      1680
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264 agccgggagg cggcgggtgga ggcgggtggc gtggcggggg cggcggcggg ggtgtttcgt      1800
266 cggagaagtc gggattccgg gtaccgagcg ccacctgcca gccattcacg ccaggacag      1860
268 gcagcccgag ctccagcgcc tcggcctgct cgccgggagg tatgctgtcc tcggccgggg      1920

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270 gtgccccgga gggcaaggac gacaagaaag acaccgacgt gggcggcggt ggcaagggca 1980
272 ccggggggcgc ctcgcccgaa gggggaccca cggggctggc acacggccgg attagctgcg 2040
274 gcggcggggat taatgtggat gtgaaccagc atccggatgg gggcccggga ggcaaggctc 2100
276 tgggctcgga ctgcggcggt tcatcgggct ccagctccgg ctccggcccc agcgcgccca 2160
278 cctcctcctc agtggtgggc tctgggctgg tggctcccgt gtcaccctac aagccggggc 2220
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286 cggccggctc cagccctttg gccggagcgt ctccgccgtc cgtgatgaca gccagtttgt 2460
288 gccgggaccc ttactgcctc agctaccact gcgctagcca cctggcaggg gcggcgccg 2520
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336 gaacacttaa ctatttttaa tttttaagtc caccgcgtga gaaggggaca aggtttacgt 3960
338 catgtactaa aataatagac aatgtatcgc tttaaagatt aaaattccgt atatttgatg 4020
340 taaaaaaaaa aaaaacaaaa aacaaaaaac acttttgtgg cgcgcttgag cctggagaaa 4080
342 agtggttaga aacacattgc gtattggggc gcggggcccc atgatggata agatgacaca 4140
344 ggtgcacaaa gcagtgtccc aagaaagacc cgcggaacag acacagaggg gtaggggaat 4200
346 ccacacgaaa aaaaaagccc cgggggggaca accagagggt tctgagagaa ccccaaaggg 4260
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350 ttgcc 4325

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353 &lt;210&gt; SEQ ID NO: 4

354 &lt;211&gt; LENGTH: 619

355 &lt;212&gt; TYPE: PRT

356 &lt;213&gt; ORGANISM: Homo sapiens

358 &lt;400&gt; SEQUENCE: 4

360 Met Leu Leu Gly Val Val Val Gly Arg Gly Glu Gln Ser Ala Ala Phe

361 1 5 10 15

364 Pro Asn Gly Glu Asn Val Cys Glu Trp Val Leu Lys Arg Gly Cys Arg



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365			20			25			30								
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369			35			40			45								
372	Glu	Ala	Phe	Glu	Pro	Gln	Lys	Pro	Gly	Phe	Tyr	Lys	Gly	Phe	His	Phe	
373		50				55			60								
376	Phe	Leu	Cys	Val	Thr	Leu	Pro	Pro	His	Arg	Leu	Thr	Pro	Gln	Leu	Asp	
377	65					70			75							80	
380	Ala	Lys	Lys	Ser	Pro	Leu	Ala	Leu	Leu	Ala	Gln	Thr	Cys	Ser	Gln	Ile	
381					85				90						95		
384	Gly	Lys	Pro	Asp	Pro	Ser	Pro	Ser	Ser	Lys	Leu	Ser	Ser	Val	Ala	Ser	
385				100					105					110			
388	Asn	Gly	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Gly	Ala	Ala	Gly	Asp	Lys	
389			115					120					125				
392	Asp	Thr	Lys	Ser	Gly	Pro	Leu	Lys	Leu	Ser	Asp	Ile	Gly	Val	Glu	Asp	
393		130					135					140					
396	Lys	Ser	Ser	Phe	Lys	Pro	Tyr	Ser	Lys	Pro	Gly	Ser	Asp	Lys	Lys	Glu	
397	145					150					155					160	
400	Pro	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
401					165				170						175		
404	Gly	Val	Ser	Ser	Glu	Lys	Ser	Gly	Phe	Arg	Val	Pro	Ser	Ala	Thr	Cys	
405				180					185					190			
408	Gln	Pro	Phe	Thr	Pro	Arg	Thr	Gly	Ser	Pro	Ser	Ser	Ser	Ala	Ser	Ala	
409			195					200					205				
412	Cys	Ser	Pro	Gly	Gly	Met	Leu	Ser	Ser	Ala	Gly	Gly	Ala	Pro	Glu	Gly	
413		210					215				220						
416	Lys	Asp	Asp	Lys	Lys	Asp	Thr	Asp	Val	Gly	Gly	Gly	Gly	Lys	Gly	Thr	
417	225					230				235						240	
420	Gly	Gly	Ala	Ser	Ala	Glu	Gly	Gly	Pro	Thr	Gly	Leu	Ala	His	Gly	Arg	
421				245					250					255			
424	Ile	Ser	Cys	Gly	Gly	Gly	Ile	Asn	Val	Asp	Val	Asn	Gln	His	Pro	Asp	
425			260					265					270				
428	Gly	Gly	Pro	Gly	Gly	Lys	Ala	Leu	Gly	Ser	Asp	Cys	Gly	Gly	Ser	Ser	
429			275					280				285					
432	Gly	Ser	Ser	Ser	Gly	Ser	Gly	Pro	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Val	
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436	Leu	Gly	Ser	Gly	Leu	Val	Ala	Pro	Val	Ser	Pro	Tyr	Lys	Pro	Gly	Gln	
437	305					310				315						320	
440	Thr	Val	Phe	Pro	Leu	Pro	Pro	Ala	Gly	Met	Thr	Tyr	Pro	Gly	Ser	Leu	
441				325					330					335			
444	Ala	Gly	Ala	Tyr	Ala	Gly	Tyr	Pro	Pro	Gln	Phe	Leu	Pro	His	Gly	Val	
445			340					345					350				
448	Ala	Leu	Asp	Pro	Thr	Lys	Pro	Gly	Ser	Leu	Val	Gly	Ala	Gln	Leu	Ala	
449			355					360				365					
452	Ala	Ala	Ala	Ala	Gly	Ser	Leu	Gly	Cys	Ser	Lys	Pro	Ala	Gly	Ser	Ser	
453		370					375					380					
456	Pro	Leu	Ala	Gly	Ala	Ser	Pro	Pro	Ser	Val	Met	Thr	Ala	Ser	Leu	Cys	
457	385					390				395						400	
460	Arg	Asp	Pro	Tyr	Cys	Leu	Ser	Tyr	His	Cys	Ala	Ser	His	Leu	Ala	Gly	
461				405					410					415			

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 546  
Seq#:21; N Pos. 13,20,34,53,59  
Seq#:22; Xaa Pos. 3,5,10,16,18

**VERIFICATION SUMMARY**

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:540  
L:2962 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0  
L:3078 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0  
M:341 Repeated in SeqNo=22